

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:20:40 ; Search time 7.9771 Seconds
(without alignments)
228.975 Million cell updates/sec

Title: US-09-787-082-9

Perfect score: 119

Sequence: 1 CCNPNVCHLEHSLNCTGG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	80.7	16	2 A59046	alpha-conotoxin MII
2	54	45.4	160	2 T25185	hypothetical prote
3	49.5	41.6	151	2 T20071	hypothetical prote
4	49	41.2	399	2 T83888	hypothetical wd-40
5	48.5	40.8	644	2 A36325	epidermal growth f
6	48.5	40.8	894	2 T27007	hypothetical prote
7	48.5	40.8	1210	2 A53183	epidermal growth f
8	48	40.3	16	2 A59042	alpha-conotoxin Ep
9	48	40.3	379	2 T16213	APX-1 protein homo
10	48	40.3	589	2 B38128	epithelin/granulin
11	47	39.5	18	1 A58589	alpha-conotoxin EI
12	47	39.5	566	2 S19307	carboxylesterase (
13	46.5	39.1	728	2 I50719	C-Delta-1 - chick
14	46	38.7	54	2 A31436	ovomucoid, third d
15	45.5	38.2	159	2 T33696	hypothetical prote
16	45	37.8	16	2 A59045	alpha-conotoxin Au
17	45	37.8	506	2 S50937	hypothetical prote
18	45	37.8	878	2 B71460	probable outer mem
19	45	37.8	2907	2 A57278	fibrillin-2 precur
20	45	37.8	2918	2 A54105	fibrillin-2 precur
21	44.5	37.4	294	2 T23682	hypothetical prote
22	44.5	37.4	434	2 C27827	S-locus-specific g
23	44.5	37.4	686	2 JC7569	Delta-4 protein -
24	44.5	37.4	1101	2 T16840	hypothetical prote
25	44.5	37.4	1203	2 A49175	Watch B protein -
26	44.5	37.4	2471	2 A49128	cell-fate determin
27	44	37.0	16	2 C59045	alpha-conotoxin Au
28	44	37.0	16	2 B54877	alpha-conotoxin Pn
29	44	37.0	49	2 I48946	cellular disintegr

30 44 37.0 423 2 AC3553 4-aminobutyrate tr
31 44 37.0 527 2 T01019 transport protein
32 44 37.0 689 2 T42760 fibulin, splice fo
33 44 37.0 712 2 T42990 fibulin 1, splice
34 44 37.0 798 2 T22793 hypothetical prote
35 44 37.0 1582 2 T15308 hypothetical prote
36 43.5 36.6 986 1 OYURGA spectact receptor p
37 43 36.1 124 2 AG2339 hypothetical prote
38 43 36.1 222 2 G87523 cell division App-
39 43 36.1 337 2 T18431 hypothetical prote
40 43 36.1 357 2 S23403 sperm surface prot
41 43 36.1 366 2 C87624 alcohol dehydrogen
42 43 36.1 513 2 D88991 protein apx-1 [imp
43 43 36.1 525 2 B48058 RNA-binding protei
44 43 36.1 586 2 S19381 hypothetical prote
45 43 36.1 719 2 S25237 homeotic protein H

ALIGNMENTS

RESULT 1

A59046

alpha-conotoxin MII - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: A59046

R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 7522-7528, 1996

A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine rec

A:Reference number: A59046; MUID:96205934; PMID:8631783

A:Accession: A59046

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <CAR>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin MII #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 80.7%; Score 96; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNPNVCHLEHSLNLC 15
|||||
DB 2 CCNPNVCHLEHSLNLC 16

RESULT 2

T25185

hypothetical protein T23F6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25185

R:Lilovd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19992

A:Accession: T25185

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-160 <WIL>

A:Cross-references: EMBL:283127; PIDN:CAB05630.1; GSPDB:GN00022; CESP:T23F6.1

A:Experimental source: clone T23F6

C:Genetics:

A:Gene: CESP:T23F6.1

A:Map position: 4

A:Introns: 76/3; 124/3

Query Match

Best Local Similarity 45.4%; Score 54; DB 2; Length 160;

Matches 10; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

A:Molecule type: mRNA
A:Residues: 1-589 <PRO>
A:Cross-references: GB:X62322; NID:g56108; PIDN:CA44198.1; PID:g56109
R:Shoyab, M.; McDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
A:Title: Epithelins 1 and 2: isolation and characterization of two cysteine
A:Reference number: A36199; MUID:91045907; PMID:2236009
A:Accession: A36199
A:Molecule type: protein
A:Residues: 280-300 <SHO>
A:Accession: B36199
A:Molecule type: protein
A:Residues: 205-226 <SH2>
R:Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990
A:Title: Granulins, a novel class of peptide from leukocytes.
A:Reference number: A36698; MUID:91097544; PMID:2268320
A:Accession: E36698
A:Molecule type: protein
A:Residues: 279-307, 'SB', 310-324, 'T', 326, 'X', 328, 'Q' <BAT>
R:Bhandari, V.; Gaid, A.; Bateman, A.
Endocrinology 133, 2682-2689, 1993
A:Title: The complementary deoxyribonucleic acid sequence, tissue distribut
A:Reference number: I53272; MUID:94062640; PMID:8243292
A:Accession: I53272
A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA

A:Residues: 1-200,'S',203-388,'M',390-589 <RES>

A:Cross-references: GB:M97750; NID:g204223; PIDN:AAAL6903.1; PID:g204224

C:Superfamily: granulin

Query Match 40.3%; Score 48; DB 2; Length 589;

Best Local Similarity 45.0%; Pred. No. 55;

Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 CCSNP-VCHLEHSLNLTNG 18

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Db 386 CCPIEAVCCLDHQHCCPG 405

RESULT 11

A58589

A:Superfamily: alpha-conotoxin EI - cone shell (Conus ermineus)

C:Species: Conus ermineus (ermine cone)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A58589

R:Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;

Biochemistry 34, 14519-14526, 1995

A:Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nove

A:Reference number: A58589; MUID:96062516; PMID:7578057

A:Accession: A58589

A:Molecule type: protein

A:Residues: 1-18 <MAR>

A:Note: sequence confirmed by chemical synthesis

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos

F:3/Modified site: 4-hydroxyproline (Pro) #status experimental

F:4-10,5-18/Disulfide bonds: #status experimental

F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match

Best Local Similarity 39.5%; Score 47; DB 1; Length 18;

Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCSNPVCHLEHSLNLC 15

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Db 4 CCYHPTCNMSNPQIC 18

RESULT 12

S19307

A:Superfamily: carboxylesterase (EC 3.1.1.1) precursor - pig

N:Alternate names: proline-beta-naphthylamidase

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1999

C:Accession: S19307; S23607

R:Matsushima, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Mikl, K.; Kurokawa, K.; Takahash

FEBs Lett. 293, 37-41, 1991

A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-n

A:Reference number: S19307; MUID:92070571; PMID:1959668

A:Accession: S19307

A:Molecule type: mRNA

A:Residues: 1-566 <MAT>

A:Cross-references: EMBL:X63323; NID:g1930; PIDN:CAA44929.1; PID:g1931

A:Accession: S23607

A:Molecule type: protein

A:Residues: 19-40 <MAT2>

A:Note: 28-Lys and 33-Leu were also found

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-566/Product: carboxylesterase #status experimental <MAT>

F:51-552/Domain: cholinesterase homology <CHE>

F:80/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:222,467/Active site: Ser, His #status predicted

Query Match

Best Local Similarity 39.5%; Score 47; DB 2; Length 566;

Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCSNPVCHLEHSLNLTNG 18

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Db 88 CCODPVVEQMTSDLFTNG 105

RESULT 13

I50719

C:Delta-1 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Aug-2002

C:Accession: I50719

R:Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.

Nature 375, 787-790, 1995

A:Title: Expression of a Delta homologue in prospective neurons in the chick.

A:Reference number: I50719; MUID:95319507; PMID:7596411

A:Accession: I50719

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-728 <HENS>

A:Cross-references: EMBL:U26590; NID:g882411; PIDN:AACS9689.1; PID:g882412

C:Superfamily: delta-4 protein; EGF homology

F:299-332/Domain: EGF homology <EGX1>

F:339-370/Domain: EGF homology <EGF1>

F:416-447/Domain: EGF homology <EGX2>

F:454-485/Domain: EGF homology <EGF>

F:492-523/Domain: EGF homology <EGF3>

Query Match

Best Local Similarity 39.1%; Score 46.5; DB 2; Length 728;

Matches 10; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 2 CSNPVCHLEHSLNLTNG 18

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Db 485 CSTPVSRCHE-NPCHNG 500

RESULT 14

A31436

A:Title: Ovomuroid - Australian darter (fragment)

C:Species: Anhinga novaehollandiae, Anhinga rufa novaehollandiae (Australian darter)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Feb-1997

C:Accession: A31436

R:Laskowski Jr., M.; Kato, I.; Ardelt, W.; Cook, J.; Denton, A.; Emple, M.W.; Kohr, W.

, A.; Wicczorek, M.

Biochemistry 26, 202-221, 1987

A:Title: Ovomuroid third domains from 100 avian species: isolation, sequences, and hy

A:Reference number: A90515; MUID:87157615; PMID:3828298

A:Accession: A31436

A:Molecule type: protein

A:Residues: 1-54 <IAS>

A:Note: the authors designate this sequence with the code OMADR3

C:Superfamily: ovomuroid; Kazal proteinase inhibitor homology

C:Keywords: egg white; glycoprotein; serine proteinase inhibitor

F:4-54/Domain: Kazal proteinase inhibitor homology <KPI>

F:6-36,14-33,22-54/Disulfide bonds: #status predicted

F:43/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 38.7%; Score 46; DB 2; Length 54;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCSNPVCHLEHSLNLC 15

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Db 8 CYPKPVCSLEYMPLC 22

RESULT 15

T33696

A:hypothetical protein F49Fl.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

Search completed: March 17, 2003, 07:27:29
Job time : 8.9771 secs

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